What is claimed is:

1. A method for modulating metabolism of fluoroquinolone resistant pathogenic bacteria comprising the step of contacting fluoroquinolone resistant pathogenic bacteria with an antibacterially effective amount of a composition comprising a gemifloxacin compound, or antibacterially effective derivatives thereof.

2. The method of claim 1 wherein said fluoroquinolone resistant pathogenic bacteria is selected from the group consisting of:

a ciprofloxacin resistant strain of *S. pneumoniae, S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae,* a trovafloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a fluoroquinolone resistant strain of *S. pneumoniae,* a fluoroquinolone resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, and a fluoroquinolone resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region.

3. A method of treating or preventing a bacterial infection by fluoroquinolone resistant pathogenic bacteria comprising the step of administering an antibacterially effective amount of a composition comprising a gemifloxacin compound to a mammal suspected of having or being at risk of having an infection with fluoroquinolone resistant pathogenic bacteria.

4. The method of claim 3 wherein said fluoroquinolone resistant pathogenic bacteria is selected from the group consisting of:

a ciprofloxacin resistant strain of *S. pneumoniae, S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae,* a trovafloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a fluoroquinolone resistant strain of *S. pneumoniae,* a fluoroquinolone resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, and a

fluoroquinolone resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region.

5. The method of claim 1 wherein said modulating metabolism is inhibiting growth of said bacteria.

6. The method of claim 1 wherein said modulating metabolism is killing said bacteria.

7. The method of claim 1 wherein said contacting said bacteria comprises the further step of introducing said composition into a mammal.

8. The method of claim 3 wherein said mammal is a human.

9. The method of claim 7 wherein said mammal is a human.

10. The method of claim 1 wherein said bacteria is selected from the group consisting of: a ciprofloxacin resistant strain of *S. pneumoniae, S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae,* a trovafloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a fluoroquinolone resistant strain of *S. pneumoniae,* a fluoroquinolone resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, and a fluoroquinolone resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region.

11. The method of claim 1 wherein said bacteria is selected from the group consisting of: a ciprofloxacin resistant strain of *S. pneumoniae, S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a ciprofloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae,* a trovafloxacin resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, a trovafloxacin resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region, a fluoroquinolone resistant strain of *S. pneumoniae,* a fluoroquinolone resistant strain of *S. pneumoniae* having a topisomerase *IV* (*parC*) mutation in the QRDR region, and

a fluoroquinolone resistant strain of *S. pneumoniae* having a DNA gyrase (*gyrA*) mutation in the QRDR region.